#6

SEQUENCE LISTING

<110> Denney, Jr., Dan W.

<120> Vaccines for Treatment of Lymphoma and Leukemia

<130> GENITOPE-06493

<140> 09/925,192
<141> 2001-08-09

<160> 80

<170> PatentIn version 3.2

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cgcccctaac tccgcccatc ccgcccctaa ctccgcccag ttccgcccat tctccgcccc 240

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aggactcgcc cctgccttgg ggaatcccag ggaccgtcgt taaactccca ctaacgtaga 180

acccagagat cgctgcgttc ccgccccctc acccgcccgc tctcgtcatc actgaggtgg 240

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<222> (88)..(741)

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Met Pro Thr Arg Ser Pro Ser Val Val
1 5

att agc gat gat gaa cca ggt tat gac cta gat ttg ttt tgt ata cct 162
Ile Ser Asp Asp Glu Pro Gly Tyr Asp Leu Asp Leu Phe Cys Ile Pro
10 15 20 25

aat cat tat gcc gag gat ttg gaa aaa gtg ttt att cct cat gga ctg 210
Asn His Tyr Ala Glu Asp Leu Glu Lys Val Phe Ile Pro His Gly Leu
30 35 40

att atg gac agg act gaa aga ctt gct cga gat gtc atg aag gag atg 258
Ile Met Asp Arg Thr Glu Arg Leu Ala Arg Asp Val Met Lys Glu Met
45 50 55

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gga ggc cat cac att gtg gcc ctc tgt gtg ctc aag ggg ggc tat aag      306
Gly Gly His His Ile Val Ala Leu Cys Val Leu Lys Gly Gly Tyr Lys
        60                  65                  70

ttc ttt gct gac ctg ctg gat tac att aaa gca ctg aat aga aat agt      354
Phe Phe Ala Asp Leu Leu Asp Tyr Ile Lys Ala Leu Asn Arg Asn Ser
    75                  80                  85

gat aga tcc att cct atg act gta gat ttt atc aga ctg aag agc tac      402
Asp Arg Ser Ile Pro Met Thr Val Asp Phe Ile Arg Leu Lys Ser Tyr
90                  95                  100                 105

tgt aat gat cag tca acg ggg gac ata aaa gtt att ggt gga gat gat      450
Cys Asn Asp Gln Ser Thr Gly Asp Ile Lys Val Ile Gly Gly Asp Asp
                110                 115                 120

ctc tca act tta act gga aag aat gtc ttg att gtt gaa gat ata att      498
Leu Ser Thr Leu Thr Gly Lys Asn Val Leu Ile Val Glu Asp Ile Ile
            125                 130                 135

gac act ggt aaa aca atg caa act ttg ctt tcc ctg gtt aag cag tac      546
Asp Thr Gly Lys Thr Met Gln Thr Leu Leu Ser Leu Val Lys Gln Tyr
        140                 145                 150

agc ccc aaa atg gtt aag gtt gca agc ttg ctg gtg aaa agg acc tct      594
Ser Pro Lys Met Val Lys Val Ala Ser Leu Leu Val Lys Arg Thr Ser
    155                 160                 165

cga agt gtt gga tac agg cca gac ttt gtt gga ttt gaa att cca gac      642
Arg Ser Val Gly Tyr Arg Pro Asp Phe Val Gly Phe Glu Ile Pro Asp
170                 175                 180                 185

aag ttt gtt gtt gga tat gcc ctt gac tat aat gag tac ttc agg aat      690
Lys Phe Val Val Gly Tyr Ala Leu Asp Tyr Asn Glu Tyr Phe Arg Asn
                190                 195                 200

ttg aat cac gtt tgt gtc att agt gaa act gga aaa gcc aaa tac aaa      738
Leu Asn His Val Cys Val Ile Ser Glu Thr Gly Lys Ala Lys Tyr Lys
            205                 210                 215

gcc taagatgagc gcaagttgaa tctgcaaata cgaggagtcc tgttgatgtt          791
Ala
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gccagtaaaa ttagcaggtg ttctagtcct gtggccatct gcctagtaaa gctttttgca   851

tgaaccttct atgaatgtta ctgttttatt tttagaaatg tcagttgctg cgtccccaga   911

cttttgattt gcactatgag cctataggcc agcctaccct ctggtagatt gtcgcttatc   971

ttgtaagaaa aacaaatctc ttaaattacc acttttaaat aataatactg agattgtatc  1031

tgtaagaagg atttaaagag aagctatatt agtttttaa ttggtatttt aatttttata  1091

tattcaggag agaaagatgt gattgatatt gttaatttag acgagtctga agctctcgat  1151

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Glu Lys Val Phe Ile Pro His Gly Leu Ile Met Asp Arg Thr Glu Arg
        35                  40                  45

Leu Ala Arg Asp Val Met Lys Glu Met Gly Gly His His Ile Val Ala
    50                  55                  60

Leu Cys Val Leu Lys Gly Gly Tyr Lys Phe Phe Ala Asp Leu Leu Asp
65                  70                  75                  80

Tyr Ile Lys Ala Leu Asn Arg Asn Ser Asp Arg Ser Ile Pro Met Thr
                85                  90                  95

Val Asp Phe Ile Arg Leu Lys Ser Tyr Cys Asn Asp Gln Ser Thr Gly
            100                 105                 110

Asp Ile Lys Val Ile Gly Gly Asp Asp Leu Ser Thr Leu Thr Gly Lys
        115                 120                 125

Asn Val Leu Ile Val Glu Asp Ile Ile Asp Thr Gly Lys Thr Met Gln
    130                 135                 140

Thr Leu Leu Ser Leu Val Lys Gln Tyr Ser Pro Lys Met Val Lys Val
145                 150                 155                 160

Ala Ser Leu Leu Val Lys Arg Thr Ser Arg Ser Val Gly Tyr Arg Pro
                165                 170                 175

Asp Phe Val Gly Phe Glu Ile Pro Asp Lys Phe Val Val Gly Tyr Ala
            180                 185                 190

Leu Asp Tyr Asn Glu Tyr Phe Arg Asn Leu Asn His Val Cys Val Ile
        195                 200                 205

Ser Glu Thr Gly Lys Ala Lys Tyr Lys Ala
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<222> (13)..(573)

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Asn Met Gly Ile Gly Lys Asn Gly Asp Leu Pro Trp Pro Pro Leu Arg
15 20 25

aac gag ttc aag tac ttc caa aga atg acc aca acc tct tca gtg gaa 147
Asn Glu Phe Lys Tyr Phe Gln Arg Met Thr Thr Thr Ser Ser Val Glu
30 35 40 45

ggt aaa cag aat ctg gtg att atg ggt agg aaa acc tgg ttc tcc att 195
Gly Lys Gln Asn Leu Val Ile Met Gly Arg Lys Thr Trp Phe Ser Ile
50 55 60

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cct gag aag aat cga cct tta aag gac aga att aat ata gtt ctc agt      243
Pro Glu Lys Asn Arg Pro Leu Lys Asp Arg Ile Asn Ile Val Leu Ser
            65                  70                  75

aga gaa ctc aaa gaa cca cca cga gga gct cat ttt ctt gcc aaa agt      291
Arg Glu Leu Lys Glu Pro Pro Arg Gly Ala His Phe Leu Ala Lys Ser
        80                  85                  90

ttg gat gat gcc tta aga ctt att gaa caa ccg gaa ttg gca agt aaa      339
Leu Asp Asp Ala Leu Arg Leu Ile Glu Gln Pro Glu Leu Ala Ser Lys
    95                  100                 105

gta gac atg gtt tgg ata gtc gga ggc agt tct gtt tac cag gaa gcc      387
Val Asp Met Val Trp Ile Val Gly Gly Ser Ser Val Tyr Gln Glu Ala
110                 115                 120                 125

atg aat caa cca ggc cac ctt aga ctc ttt gtg aca agg atc atg cag      435
Met Asn Gln Pro Gly His Leu Arg Leu Phe Val Thr Arg Ile Met Gln
                130                 135                 140

gaa ttt gaa agt gac acg ttt ttc cca gaa att gat ttg ggg aaa tat      483
Glu Phe Glu Ser Asp Thr Phe Phe Pro Glu Ile Asp Leu Gly Lys Tyr
            145                 150                 155

aaa ctt ctc cca gaa tac cca ggc gtc ctc tct gag gtc cag gag gaa      531
Lys Leu Leu Pro Glu Tyr Pro Gly Val Leu Ser Glu Val Gln Glu Glu
        160                 165                 170

aaa ggc atc aag tat aag ttt gaa gtc tac gag aag aaa gac              573
Lys Gly Ile Lys Tyr Lys Phe Glu Val Tyr Glu Lys Lys Asp
    175                 180                 185

taacaggaag atgctttcaa gttctctgct cccctcctaa agctatgcat ttttataaga    633

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<400> 19

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            20                  25                  30

Lys Tyr Phe Gln Arg Met Thr Thr Thr Ser Ser Val Glu Gly Lys Gln
        35                  40                  45

Asn Leu Val Ile Met Gly Arg Lys Thr Trp Phe Ser Ile Pro Glu Lys
    50                  55                  60

Asn Arg Pro Leu Lys Asp Arg Ile Asn Ile Val Leu Ser Arg Glu Leu
65                  70                  75                  80
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Lys Glu Pro Pro Arg Gly Ala His Phe Leu Ala Lys Ser Leu Asp Asp
85 90 95

Ala Leu Arg Leu Ile Glu Gln Pro Glu Leu Ala Ser Lys Val Asp Met
100 105 110

Val Trp Ile Val Gly Gly Ser Ser Val Tyr Gln Glu Ala Met Asn Gln
115 120 125

Pro Gly His Leu Arg Leu Phe Val Thr Arg Ile Met Gln Glu Phe Glu
130 135 140

Ser Asp Thr Phe Phe Pro Glu Ile Asp Leu Gly Lys Tyr Lys Leu Leu
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Lys Tyr Lys Phe Glu Val Tyr Glu Lys Lys Asp
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taggcatcga attc 134

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acttcaggta ctacccgtct tctatctggg cacacgtgtt tcacgttgac aggtttgctt 180

gggacgctag taaccatggg cttgctgact taggcatcga attcatcaag cttatcgata 240

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<220>
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<400> 25
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<210> 26
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<222> (1)..(744)

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1               5                   10                  15

ctg atg agc gct cag gaa tca tgg gct atc aaa gaa gaa cat gtg atc       96
Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile
            20                  25                  30

atc cag gcc gag ttc tat ctg aat cct gac caa tca ggc gag ttt atg      144
Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met
        35                  40                  45

ttt gac ttt gat ggt gat gag att ttc cat gtg gat atg gca aag aag      192
Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys
    50                  55                  60

gag acg gtc tgg cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag      240
Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu
65                  70                  75                  80

gct caa ggt gca ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa      288
Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu
                85                  90                  95

atc atg aca aag cgc tcc aac tat act ccg atc acc aat gta cct cca      336
Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro
            100                 105                 110

gag gta act gtg ctc acg aac agc cct gtg gaa ctg aga gag ccc aac      384
Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn
        115                 120                 125

gtc ctc atc tgt ttc ata gac aag ttc acc cca cca gtg gtc aat gtc      432
Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val
    130                 135                 140

acg tgg ctt cga aat gga aaa cct gtc acc aca gga gtg tca gag aca      480
Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr
145                 150                 155                 160

gtc ttc ctg ccc agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc      528
Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu
                165                 170                 175

ccc ttc ctg ccc tca act gag gac gtt tac gac tgc agg gtg gag cac      576
Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His
            180                 185                 190
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Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro
        195                 200                 205

agc cct ctc cca aat aaa gga agt gga acc act tca ggt act acc cgt      672
Ser Pro Leu Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg
    210                 215                 220

ctt cta tct ggg cac acg tgt ttc acg ttg aca ggt ttg ctt ggg acg      720
Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr
225                 230                 235                 240

cta gta acc atg ggc ttg ctg act tag                                  747
Leu Val Thr Met Gly Leu Leu Thr
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            20                  25                  30

Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met
        35                  40                  45

Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys
    50                  55                  60

Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu
65                  70                  75                  80

Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu
                85                  90                  95

Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro
            100                 105                 110

Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn
        115                 120                 125

Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val
    130                 135                 140
```

```
Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr
145                 150                 155                 160

Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu
                165                 170                 175

Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His
            180                 185                 190

Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro
        195                 200                 205

Ser Pro Leu Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg
    210                 215                 220

Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr
225                 230                 235                 240

Leu Val Thr Met Gly Leu Leu Thr
                245
```

<210> 28
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 28
ccacttcctt tatttggtgc agattcag 28

<210> 29
<211> 786
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> CDS
<222> (1)..(783)

<400> 29

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atg gtg tgt ctg aag ctc cct gga ggc tcc tgc atg aca gcg ctg aca      48
Met Val Cys Leu Lys Leu Pro Gly Gly Ser Cys Met Thr Ala Leu Thr
1               5                   10                  15

gtg aca ctg atg gtg ctg agc tcc cga ctg gct ttg gct ggg gac acc      96
Val Thr Leu Met Val Leu Ser Ser Arg Leu Ala Leu Ala Gly Asp Thr
            20                  25                  30
```

```
cga cca cgt ttc ttg tgg cag ctt aag ttt gaa tgt cat ttc ttc aat      144
Arg Pro Arg Phe Leu Trp Gln Leu Lys Phe Glu Cys His Phe Phe Asn
        35                  40                  45

ggg acg gag cgg gtg cgg ttg ctg gaa aga tgc atc tat aac caa gag      192
Gly Thr Glu Arg Val Arg Leu Leu Glu Arg Cys Ile Tyr Asn Gln Glu
    50                  55                  60

gag tcc gtg cgc ttc gac agc gac gtg ggg gag tac cgg gcg gtt gag      240
Glu Ser Val Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Glu
65                  70                  75                  80

gag ctg ggg cgg cct gat gcc gag tac tgg aac agc cag aag gac ctc      288
Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Leu
                85                  90                  95

ctg gag cag aag cgg ggc cag gtg gac aat tac tgc aga cac aac tac      336
Leu Glu Gln Lys Arg Gly Gln Val Asp Asn Tyr Cys Arg His Asn Tyr
            100                 105                 110

ggg gtt ggt gag agc ttc aca gtg cag cgg cga gtt gag cct aag gtg      384
Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val Glu Pro Lys Val
        115                 120                 125

act gtg tat cct tca aag acc cag ccc ctg cag cac cac aac ctc ctg      432
Thr Val Tyr Pro Ser Lys Thr Gln Pro Leu Gln His His Asn Leu Leu
    130                 135                 140

gtc tgc tct gtg agt ggt ttc tat cca ggc agc att gaa gtc agg tgg      480
Val Cys Ser Val Ser Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp
145                 150                 155                 160

ttc cgg aac ggc cag gaa gag aag gct ggg gtg gtg tcc acg ggc ctg      528
Phe Arg Asn Gly Gln Glu Glu Lys Ala Gly Val Val Ser Thr Gly Leu
                165                 170                 175

atc cag aat gga gat tgg acc ttc cag acc ctg gtg atg ctg gaa ata      576
Ile Gln Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met Leu Glu Ile
            180                 185                 190

gtt cct cgg agt gga gag gtt tac acc tgc caa gtg gag cac cca agt      624
Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu His Pro Ser
        195                 200                 205

gtg acg agc cct ctc aca gtg gaa tgg aga gca cgg tct gaa tct gca      672
Val Thr Ser Pro Leu Thr Val Glu Trp Arg Ala Arg Ser Glu Ser Ala
    210                 215                 220

cca aat aaa gga agt gga acc act tca ggt act acc cgt ctt cta tct      720
Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg Leu Leu Ser
225                 230                 235                 240

ggg cac acg tgt ttc acg ttg aca ggt ttg ctt ggg acg cta gta acc      768
Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu Val Thr
                245                 250                 255

atg ggc ttg ctg act tag                                             786
Met Gly Leu Leu Thr
            260
```

<210> 30
<211> 261
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 30

```
Met Val Cys Leu Lys Leu Pro Gly Gly Ser Cys Met Thr Ala Leu Thr
1               5                  10                  15

Val Thr Leu Met Val Leu Ser Ser Arg Leu Ala Leu Ala Gly Asp Thr
            20                  25                  30

Arg Pro Arg Phe Leu Trp Gln Leu Lys Phe Glu Cys His Phe Phe Asn
        35                  40                  45

Gly Thr Glu Arg Val Arg Leu Leu Glu Arg Cys Ile Tyr Asn Gln Glu
    50                  55                  60

Glu Ser Val Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Glu
65                  70                  75                  80

Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Leu
                85                  90                  95

Leu Glu Gln Lys Arg Gly Gln Val Asp Asn Tyr Cys Arg His Asn Tyr
            100                 105                 110

Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val Glu Pro Lys Val
        115                 120                 125

Thr Val Tyr Pro Ser Lys Thr Gln Pro Leu Gln His His Asn Leu Leu
    130                 135                 140

Val Cys Ser Val Ser Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp
145                 150                 155                 160

Phe Arg Asn Gly Gln Glu Glu Lys Ala Gly Val Val Ser Thr Gly Leu
                165                 170                 175

Ile Gln Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met Leu Glu Ile
            180                 185                 190

Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu His Pro Ser
        195                 200                 205
```

```
Val Thr Ser Pro Leu Thr Val Glu Trp Arg Ala Arg Ser Glu Ser Ala
    210                 215                 220

Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg Leu Leu Ser
225                 230                 235                 240

Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu Val Thr
                245                 250                 255

Met Gly Leu Leu Thr
            260
```

<210> 31
<211> 189
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> CDS
<222> (1)..(186)

<400> 31

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ttg gat cca cga tcg ttt cta ttg cgc aat cca aat gat aag tac gaa       48
Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr Glu
1               5                   10                  15

cca ttt tgg gaa gat act aca gag aac gtg gtg tgt gcc ctg ggc ctg       96
Pro Phe Trp Glu Asp Thr Thr Glu Asn Val Val Cys Ala Leu Gly Leu
            20                  25                  30

act gtg ggt ctg gtg ggc atc att att ggg acc atc ttc atc atc aag      144
Thr Val Gly Leu Val Gly Ile Ile Ile Gly Thr Ile Phe Ile Ile Lys
        35                  40                  45

gga gtg cgc aaa agc aat gca gca gaa cgc agg ggg cct ctg taa          189
Gly Val Arg Lys Ser Asn Ala Ala Glu Arg Arg Gly Pro Leu
    50                  55                  60
```

<210> 32
<211> 62
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 32

Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr Glu
1 5 10 15

Pro Phe Trp Glu Asp Thr Thr Glu Asn Val Val Cys Ala Leu Gly Leu
20 25 30

Thr Val Gly Leu Val Gly Ile Ile Ile Gly Thr Ile Phe Ile Ile Lys
35 40 45

Gly Val Arg Lys Ser Asn Ala Ala Glu Arg Arg Gly Pro Leu
50 55 60

<210> 33
<211> 192
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> CDS
<222> (1)..(189)

<400> 33
ttg gat cca cga tcg ttt cta ttg cgc aat cca aat gat aag tac gaa 48
Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr Glu
1 5 10 15

cca ttt tgg gaa gat cag agc aag atg ctg agt gga gtc ggg ggc ttc 96
Pro Phe Trp Glu Asp Gln Ser Lys Met Leu Ser Gly Val Gly Gly Phe
20 25 30

gtg ctg ggc ctg ctc ttc ctt ggg gcc ggg ctg ttc atc tac ttc agg 144
Val Leu Gly Leu Leu Phe Leu Gly Ala Gly Leu Phe Ile Tyr Phe Arg
35 40 45

aat cag aaa gga cac tct gga ctt cag cca aca gga ttc ctg agc tga 192
Asn Gln Lys Gly His Ser Gly Leu Gln Pro Thr Gly Phe Leu Ser
50 55 60

<210> 34
<211> 63
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 34

Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr Glu
1 5 10 15

Pro Phe Trp Glu Asp Gln Ser Lys Met Leu Ser Gly Val Gly Gly Phe
20 25 30

Val Leu Gly Leu Leu Phe Leu Gly Ala Gly Leu Phe Ile Tyr Phe Arg
35 40 45

Asn Gln Lys Gly His Ser Gly Leu Gln Pro Thr Gly Phe Leu Ser
50 55 60

<210> 35
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 35
cgatcgtgga tccaagttta ggttcgtatc tgtttcaaa 39

<210> 36
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 36
cgatcgagga tccaagatgg tggcagacag gacc 34

<210> 37
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 37
acgcgtccac catggccata agtggagtcc ct 32

<210> 38
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 38
ggatccaact ctgtagtctc tgggagag 28

<210> 39
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 39
acgcgtccac catggtgtgt ctgaagctcc tg 32

<210> 40
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 40
ggatccaact tgctctgtgc agattcaga 29

<210> 41
<211> 292
<212> DNA
<213> Homo sapiens

<400> 41
gaattctttt ttgcgtgtgg cagttttaag ttattagttt ttaaaatcag tacttttttaa 60

tggaaacaac ttgaccaaaa atttgtcaca gaattttgag acccattaaa aaagttaaat 120

gagaaacctg tgtgttcctt tggtcaacac cgagacattt aggtgaaaga catctaattc 180

tggttttacg aatctggaaa cttcttgaaa atgtaattct tgagttaaca cttctgggtg 240

gagaataggg ttgttttccc cccacataat tggaagggga aggaatatcg at 292

<210> 42
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 42
tcgatggcgc gccttaatta 20

<210> 43
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 43
agcttaatta aggcgcgcca 20

<210> 44
<211> 1147
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 44
gcggccgcgt cgaccaaggg ccccagcgtg ttccccctgg ccccctgctc ccgcagcacc 60

agcggcggca ccgccgccct gggctgcctg gtgaaggact acttccccga gcccgtgacc 120

gtgagctgga acagcggcgc cctgaccagc ggcgtccaca ccttccccgc cgtgctgcag 180

tccagcggcc tgtactccct gagcagcgtg gtgaccgtgc ccagcagcag cctgggcacc 240

cagacctaca cctgcaacgt gaaccacaag cccagcaaca ccaaggtgga caagcgcgtg 300

gagctgaaga cccccctggg cgacaccacc cacacctgcc cccgctgccc cgagcccaag 360

agctgcgaca cccctccccc ctgcccccgc tgccccgagc ccaagagctg cgacacccct 420

cccccctgcc cccgctgccc cgagcccaag agctgcgaca cccctccccc ctgcccccgc 480

tgccccgccc ccgagctgct gggcggcccc agcgtgttcc tgttcccccc caagcccaag 540

gacaccctga tgatctcccg cacccccgag gtgacctgcg tggtggtgga cgtgagccac 600

gaggaccccg aggtgcagtt caagtggtac gtggacggcg tggaggtgca taacgccaag 660

accaagcccc gcgaggagca gtacaacagc accttccgcg tggtgagcgt gctgaccgtg 720

ctgcaccagg actggctgaa cggcaaggag tacaagtgca aggtgagcaa caaggccctg 780

cccgccccca tcgagaagac catctccaag accaagggcc agccccgcga gccccaggtg 840

tacaccctgc cccccagccg cgaggagatg accaagaacc aggtgagcct gacctgcctg 900

gtgaagggct tctaccccag cgacatcgcc gtggagtggg agagcagcgg ccagcccgag 960

aacaactaca acaccacccc ccccatgctg gacagcgacg gcagcttctt cctgtacagc 1020

aagctgaccg tggacaagag ccgctggcag cagggcaaca tcttctcctg cagcgtgatg 1080

catgaggccc tgcacaaccg cttcacccag aagagcctga gcctgagccc cggcaagtga 1140

tagatct 1147

<210> 45
<211> 377
<212> PRT
<213> Homo sapiens

<400> 45

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1               5                  10                  15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                  70                  75                  80

Tyr Thr Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro
            100                 105                 110

Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg
        115                 120                 125

Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys
    130                 135                 140

Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
145                 150                 155                 160

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                165                 170                 175

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            180                 185                 190

Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr
        195                 200                 205

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    210                 215                 220
```

```
Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His
225                 230                 235                 240

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                245                 250                 255

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
            260                 265                 270

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
        275                 280                 285

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    290                 295                 300

Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn
305                 310                 315                 320

Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
                325                 330                 335

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
            340                 345                 350

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
        355                 360                 365

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    370                 375
```

<210> 46
<211> 999
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 46
gcggccgcgc gtcgaccaag ggccccagcg tgttcccct ggccccctgc agccgcagca 60

ccagcgagag caccgccgcc ctgggctgcc tggtgaagga ctacttcccc gagcccgtga 120

ccgtgagctg gaacagcggc gccctgacca gcggcgtgca caccttcccc gccgtgctgc 180

agagcagcgg cctgtactcc ctgagcagcg tggtgaccgt gcccagcagc agcctgggca 240

ccaagaccta cacctgcaac gtggaccaca agcccagcaa caccaaggtg gacaagcgcg 300

tggagagcaa gtacggcccc ccctgcccca gctgccccgc ccccgagttc ctgggcggcc 360

ccagcgtgtt cctgttcccc cccaagccca aggacaccct gatgatcagc cgcacccccg 420

aggtgacctg cgtggtggtg gacgtgagcc aggaggaccc cgaggtgcag ttcaactggt 480

acgtggacgg cgtggaggtg cataacgcca agaccaagcc ccgcgaggag cagttcaaca 540

gcacctaccg cgtggtgagc gtgctgaccg tgctgcacca ggactggctg aacggcaagg 600

agtacaagtg caaggtgtcc aacaagggcc tgcccagcag catcgagaag accatcagca 660

aggccaaggg ccagccccgc gagccccagg tgtacaccct gccccccagc caggaggaga 720

tgaccaagaa ccaggtgagc ctgacctgcc tggtgaaggg cttctacccc agcgacatcg 780

ccgtggagtg ggagagcaac ggccagcccg agaacaacta caagaccacc cccccgtgc 840

tggacagcga cggcagcttc ttcctgtaca gccgcctgac cgtggacaag agccgctggc 900

aggagggcaa cgtgttctcc tgctccgtga tgcatgaggc cctgcacaac cactacaccc 960

agaagagcct gagcctgagc ctgggcaagt gatagatct 999

<210> 47
<211> 327
<212> PRT
<213> Homo sapiens

<400> 47

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1 5 10 15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro
100 105 110

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
115 120 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
130 135 140

```
Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145                 150                 155                 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
                165                 170                 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
            180                 185                 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
        195                 200                 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
    210                 215                 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225                 230                 235                 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
                245                 250                 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
            260                 265                 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
        275                 280                 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
    290                 295                 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305                 310                 315                 320

Leu Ser Leu Ser Leu Gly Lys
                325
```

<210> 48
<211> 337
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 48
gcggccgcac tgtggctgca ccatctgtct tcatcttccc gccatctgat gagcagctta 60

agtccggaac cgccagcgtg gtgtgcctgc tgaacaactt ctacccccgc gaggccaagg 120

tgcagtggaa ggtggacaac gccctccaga gcggcaactc ccaggagagc gtgaccgagc 180

aggacagcaa ggacagcacc tacagcctga gcagcaccct gaccctgagc aaggccgact 240

acgagaagca caaggtgtac gcctgcgagg tgacccatca gggcctgagc agccccgtga 300

ccaagagctt caaccggggc gagtgctagt gagatct 337

<210> 49
<211> 106
<212> PRT
<213> Homo sapiens

<400> 49

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
20 25 30

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
35 40 45

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65 70 75 80

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 50
<211> 346
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 50
gcggccgcac cgtcctaggt cagcccaagg cggcgcccag cgtgaccctg ttcccccca 60

gcagcgagga gctgcaggcc aacaaggcca ccctggtgtg cctgatcagc gacttctacc 120

ccggggccgt gaccgtggcc tggaaggccg acagcagccc cgtgaaggcc ggcgtggaga 180

ccaccacccc cagcaagcag agcaacaaca agtacgccgc cagcagctac ctgagcctga 240

cccccgagca gtggaagagc caccgcagct acagctgcca ggtcacccac gagggcagca 300

ccgtggagaa gaccgtggcc cccaccgagt gcagctagtg agatct 346

<210> 51
<211> 109
<212> PRT
<213> Homo sapiens

<400> 51

Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro
1 5 10 15

Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu
20 25 30

Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp
35 40 45

Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln
50 55 60

Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu
65 70 75 80

Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly
85 90 95

Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
100 105

<210> 52
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 52
tctagaattc acgcgtccac catggactgg acctggag 38

<210> 53
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 53
tctagaattc acgcgtccac catggacaca ctttgctaca c 41

<210> 54
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 54
tctagaattc acgcgtccac catggagttt gggctgagct gg 42

<210> 55
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 55
tctagaattc acgcgtccac catgaaacac ctgtggttct tcct 44

<210> 56
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 56
tctagaattc acgcgtccac catggggtca accgccatcc t 41

<210> 57
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 57
tctagaattc acgcgtccac catgtctgtc tccttcctca tctt 44

<210> 58
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 58
gcctgagttc cacgacaccg tcac 24

<210> 59
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 59
ggggaaaagg gttggggcgg atgc 24

<210> 60
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 60
gaggggccct tggtcgacgc tgaggagacg gtgaccagg 39

<210> 61
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 61
gaggggccct tggtcgacgc tgaagagacg gtgaccattg 40

<210> 62
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 62
gaggggccct tggtcgacgc tgaggagacg gtgaccgtg 39

<210> 63
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 63
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<210> 78
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<220>
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<222> (17)..(17)
<223> n is a, c, g, or t

<220>
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<220>
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<400> 78
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